

SEQUENCE LISTING

<110> Takeda Chemical Industries, Ltd.

<120> Novel G Protein Coupled Receptor Protein and Its Use

5 <130> 2633WOOP

<150> JP 11-241530

<151> 1999-08-27

<160> 7

<210> 1

10 <211> 431

<212> PRT

<213> Human

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Pro Leu Val Tyr Thr Pro Glu Leu Pro Gly Arg Ala Lys Leu Ala Leu

 35 40 45

20 Val Leu Thr Gly Val Leu Ile Phe Ala Leu Ala Leu Phe Gly Asn Ala

 50 55 60

Leu Val Phe Tyr Val Val Thr Arg Ser Lys Ala Met Arg Thr Val Thr

 65 70 75 80

Asn Ile Phe Ile Cys Ser Leu Ala Leu Ser Asp Leu Leu Ile Thr Phe

25 85 90 95

Phe Cys Ile Pro Val Thr Met Leu Gln Asn Ile Ser Asp Asn Trp Leu

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	Gln Gly Leu Val His Pro Phe Lys Met Lys Trp Gln Tyr Thr Asn Arg		
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	Arg Ala Phe Thr Met Leu Gly Val Val Trp Leu Val Ala Val Ile Val		
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	Leu Tyr Glu Lys Glu His Ile Cys Cys Leu Glu Glu Trp Thr Ser Pro		
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	Val His Gln Lys Ile Tyr Thr Thr Phe Ile Leu Val Ile Leu Phe Leu		
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	Leu Pro Leu Met Val Met Leu Ile Leu Tyr Ser Lys Ile Gly Tyr Glu		
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	Leu Trp Ile Lys Lys Arg Val Gly Asp Gly Ser Val Leu Arg Thr Ile		
	245	250	255
20	His Gly Lys Glu Met Ser Lys Ile Ala Arg Lys Lys Lys Arg Ala Val		
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	Ile Met Met Val Thr Val Val Ala Leu Phe Ala Val Cys Trp Ala Pro		
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	Phe His Val Val His Met Met Ile Glu Tyr Ser Asn Phe Glu Lys Glu		
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	Tyr Asp Asp Val Thr Ile Lys Met Ile Phe Ala Ile Val Gln Ile Ile		

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 Glu Asn Phe Lys Lys Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val
 5 340 345 350
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 355 360 365
 Met Met Arg Lys Lys Ala Lys Phe Ser Leu Arg Glu Asn Pro Val Glu
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 10 Glu Thr Lys Gly Glu Ala Phe Ser Asp Gly Asn Ile Glu Val Lys Leu
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 25 AACATCTTTA TCTGCTCCTT GCGGCTCAGT GACCTGCTCA TCACCTTCTT CTGCATTCCC 300
 GTCACCATGC TCCAGAACAT TTCCGACAAC TGGCTGGGGG GTGCTTTCAT TTGCAAGATG 360

GTGCCATTTG TCCAGTCTAC CGCTGTTGTG ACAGAAATCC TCACTATGAC CTGCATTGCT 420
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AGGGCTTTCA CAATGCTAGG TGTGGTCTGG CTGGTGGCAG TCATCGTAGG ATCACCCATG 540
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ATCCTCTTCC TCCTGCCTCT TATGGTGATG CTTATTCTGT ACAGTAAAT TGGTTATGAA 720
CTTTGGATAA AGAAAAGAGT TGGGGATGGT TCAGTGCTTC GAACTATTCA TGGAAAAGAA 780
ATGTCCAAAA TAGCCAGGAA GAAGAAACGA GCTGTCATTA TGATGGTGAC AGTGGTGGCT 840
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10 TTTGAAAAGG AATATGATGA TGTCACAATC AAGATGATTT TTGCTATCGT GCAAATTATT 960
GGATTTTCCA ACTCCATCTG TAATCCCATT GTCTATGCAT TTATGAATGA AAACCTTCAA 1020
AAAAATGTTT TGTCTGCAGT TTGTTATTGC ATAGTAAATA AAACCTTCTC TCCAGCACAA 1080
AGGCATGGAA ATTCAGGAAT TACAATGATG CGGAAGAAAG CAAAGTTTTC CCTCAGAGAG 1140
AATCCAGTGG AGGAAACCAA AGGAGAAGCA TTCAGTGATG GCAACATTGA AGTCAAATTG 1200
15 TGTGAACAGA CAGAGGAGAA GAAAAAGCTC AAACGACATC TTGCTCTCTT TAGGTCTGAA 1260
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20 <213> Artificial Sequence

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20 <223>
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<210> 7
<211> 26
25 <212> DNA
<213> Artificial Sequence

SEQUENCE LISTING

<110> WATANABE, TAKUYA
 KIKUCHI, KUNIKO
 SHINTANI, YASUSHI

<120> NOVEL G PROTEIN-COUPLED RECEPTOR PROTEIN
 AND DNA THEREOF

<130> 57132(46342)

<140> 10/070,241

<141> 2002-02-27

<150> JP 11-241530

<151> 1999-08-27

<160> 7

<210> 1

<211> 431

<212> PRT

<213> Homo sapiens

<400> 1

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Pro	Leu	Val	Tyr	Thr	Pro	Glu	Leu	Pro	Gly	Arg	Ala	Lys	Leu	Ala	Leu	35	40	45	
Val	Leu	Thr	Gly	Val	Leu	Ile	Phe	Ala	Leu	Ala	Leu	Phe	Gly	Asn	Ala	50	55	60	
Leu	Val	Phe	Tyr	Val	Val	Thr	Arg	Ser	Lys	Ala	Met	Arg	Thr	Val	Thr	65	70	75	80
Asn	Ile	Phe	Ile	Cys	Ser	Leu	Ala	Leu	Ser	Asp	Leu	Leu	Ile	Thr	Phe	85	90	95	
Phe	Cys	Ile	Pro	Val	Thr	Met	Leu	Gln	Asn	Ile	Ser	Asp	Asn	Trp	Leu	100	105	110	
Gly	Gly	Ala	Phe	Ile	Cys	Lys	Met	Val	Pro	Phe	Val	Gln	Ser	Thr	Ala	115	120	125	
Val	Val	Thr	Glu	Ile	Leu	Thr	Met	Thr	Cys	Ile	Ala	Val	Glu	Arg	His	130	135	140	
Gln	Gly	Leu	Val	His	Pro	Phe	Lys	Met	Lys	Trp	Gln	Tyr	Thr	Asn	Arg	145	150	155	160
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SEQUENCE LISTING

- 110 · Takeda Chemical Industries, Ltd.
- 120 · Novel G Protein Coupled Receptor Protein and Its Use
- 130 · 2633W00P
- 150 · JP 11-241530
- 151 · 1999-08-27
- 160 · 7
- 210 · 1
- 211 · 431
- 212 · PRT
- 213 · Human
- 400 · 1

Met Gln Ala Leu Asn Ile Thr Pro Glu Gln Phe Ser Arg Leu Leu Arg			
1	5	10	15
Asp His Asn Leu Thr Arg Glu Gln Phe Ile Ala Leu Tyr Arg Leu Arg			
20	25	30	
Pro Leu Val Tyr Thr Pro Glu Leu Pro Gly Arg Ala Lys Leu Ala Leu			
35	40	45	
Val Leu Thr Gly Val Leu Ile Phe Ala Leu Ala Leu Phe Gly Asn Ala			
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Leu Val Phe Tyr Val Val Thr Arg Ser Lys Ala Met Arg Thr Val Thr			
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Asn Ile Phe Ile Cys Ser Leu Ala Leu Ser Asp Leu Leu Ile Thr Phe			
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Phe Cys Ile Pro Val Thr Met Leu Gln Asn Ile Ser Asp Asn Trp Leu			

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Gly Gly Ala Phe Ile Cys Lys Met Val Pro Phe Val Gln Ser Thr Ala			
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Val Val Thr Glu Ile Leu Thr Met Thr Cys Ile Ala Val Glu Arg His			
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Gln Gly Leu Val His Pro Phe Lys Met Lys Trp Gln Tyr Thr Asn Arg			
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Leu Tyr Glu Lys Glu His Ile Cys Cys Leu Glu Glu Trp Thr Ser Pro			
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Val His Gln Lys Ile Tyr Thr Thr Phe Ile Leu Val Ile Leu Phe Leu			
210	215	220	
Leu Pro Leu Met Val Met Leu Ile Leu Tyr Ser Lys Ile Gly Tyr Glu			
225	230	235	240
Leu Trp Ile Lys Lys Arg Val Gly Asp Gly Ser Val Leu Arg Thr Ile			
245	250	255	
His Gly Lys Glu Met Ser Lys Ile Ala Arg Lys Lys Lys Arg Ala Val			
260	265	270	
Ile Met Met Val Thr Val Val Ala Leu Phe Ala Val Cys Trp Ala Pro			
275	280	285	
Phe His Val Val His Met Met Ile Glu Tyr Ser Asn Phe Glu Lys Glu			
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Tyr Asp Asp Val Thr Ile Lys Met Ile Phe Ala Ile Val Gln Ile Ile			

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Glu Asn Phe Lys Lys Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val			
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	370	375	380
Glu Thr Lys Gly Glu Ala Phe Ser Asp Gly Asn Ile Glu Val Lys Leu			
385	390	395	400
Cys Glu Gln Thr Glu Glu Lys Lys Lys Leu Lys Arg His Leu Ala Leu			
	405	410	415
Phe Arg Ser Glu Leu Ala Glu Asn Ser Pro Leu Asp Ser Gly His			
	420	425	430

· 210 · 2

· 211 · 1293

· 212 · DNA

· 213 · Human

· 400 · 2

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CCGGGACGCG CCAAGCTGGC CCTCGTGCTC ACCGGCGTGC TCATCTTCGC CCTGGCGCTC	180
TTTGGCAATG CTCTGGTGTT CTACGTGGTG ACCCGCAGCA AGGCCATGCG CACCGTCACC	240
AACATCTTTA TCTGCTCCTT GCGGCTCAGT GACCTGCTCA TCACCTTCTT CTGCATTCCC	300
GTCACCATGC TCCAGAACAT TTCCGACAAC TGGCTGGGGG GTGCTTTCAT TTGCAAGATG	360

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211 37

212 DNA

213 Artificial Sequence

220

223

400 3

TGTCAGCATG CAGGCGCTTA ACATTACCCC GGAGCAG 37

210 4

211 37

·212· DNA

·213· Artificial Sequence

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GACTAGTTTA ATGCCCACTG TCTAAAGGAG AATTCTC 37

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·211· 22

·212· DNA

·213· Artificial Sequence

·220·

·223·

·400· 5

CAATGCTAGG TGTGGTCTGG CT 22

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·212· DNA

·213· Artificial Sequence

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·400· 6

GATCTCAAGT TGTGACAGT GC 22

·210· 7

·211· 26

·212· DNA

·213· Artificial Sequence

· 220 ·

· 223 ·

· 400 · 7

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 225 230 235 240
 Leu Trp Ile Lys Lys Arg Val Gly Asp Gly Ser Val Leu Arg Thr Ile
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 His Gly Lys Glu Met Ser Lys Ile Ala Arg Lys Lys Lys Arg Ala Val
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Val Thr Glu Ile Leu Thr Met Thr Cys Ile Ala Val Glu Arg His Gln	
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gat gat gtc aca atc aag atg att ttt gct atc gtg caa att att gga	1316
Asp Asp Val Thr Ile Lys Met Ile Phe Ala Ile Val Gln Ile Ile Gly	
310 315 320	
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Phe Ser Asn Ser Ile Cys Asn Pro Ile Val Tyr Ala Phe Met Asn Glu	
325 330 335	

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 340 345 350
 aaa acc ttc tct cca gca caa agg cat gga aat tca gga att aca atg 1460
 Lys Thr Phe Ser Pro Ala Gln Arg His Gly Asn Ser Gly Ile Thr Met
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 acc aaa gga gaa gca ttc agt gat ggc aac att gaa gtc aaa ttg tgt 1556
 Thr Lys Gly Glu Ala Phe Ser Asp Gly Asn Ile Glu Val Lys Leu Cys
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 gaa cag aca gag gag aag aaa aag ctc aaa cga cat ctt gct ctc ttt 1604
 Glu Gln Thr Glu Glu Lys Lys Lys Leu Lys Arg His Leu Ala Leu Phe
 405 410 415
 agg tct gaa ctg gct gag aat tct cct tta gac agt ggg cat 1646
 Arg Ser Glu Leu Ala Glu Asn Ser Pro Leu Asp Ser Gly His
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 ttttgagcaa aggtcaaata ctcttttaat tcttaagatg atgacaagaa gaaaacaaat 1766
 catgtttcca ttaaaaaatg acacgaggct agtccaagtg cagtgatgtt tacaaccaat 1826
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<210> 3

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<223> Description of Artificial Sequence: Primer

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probe

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